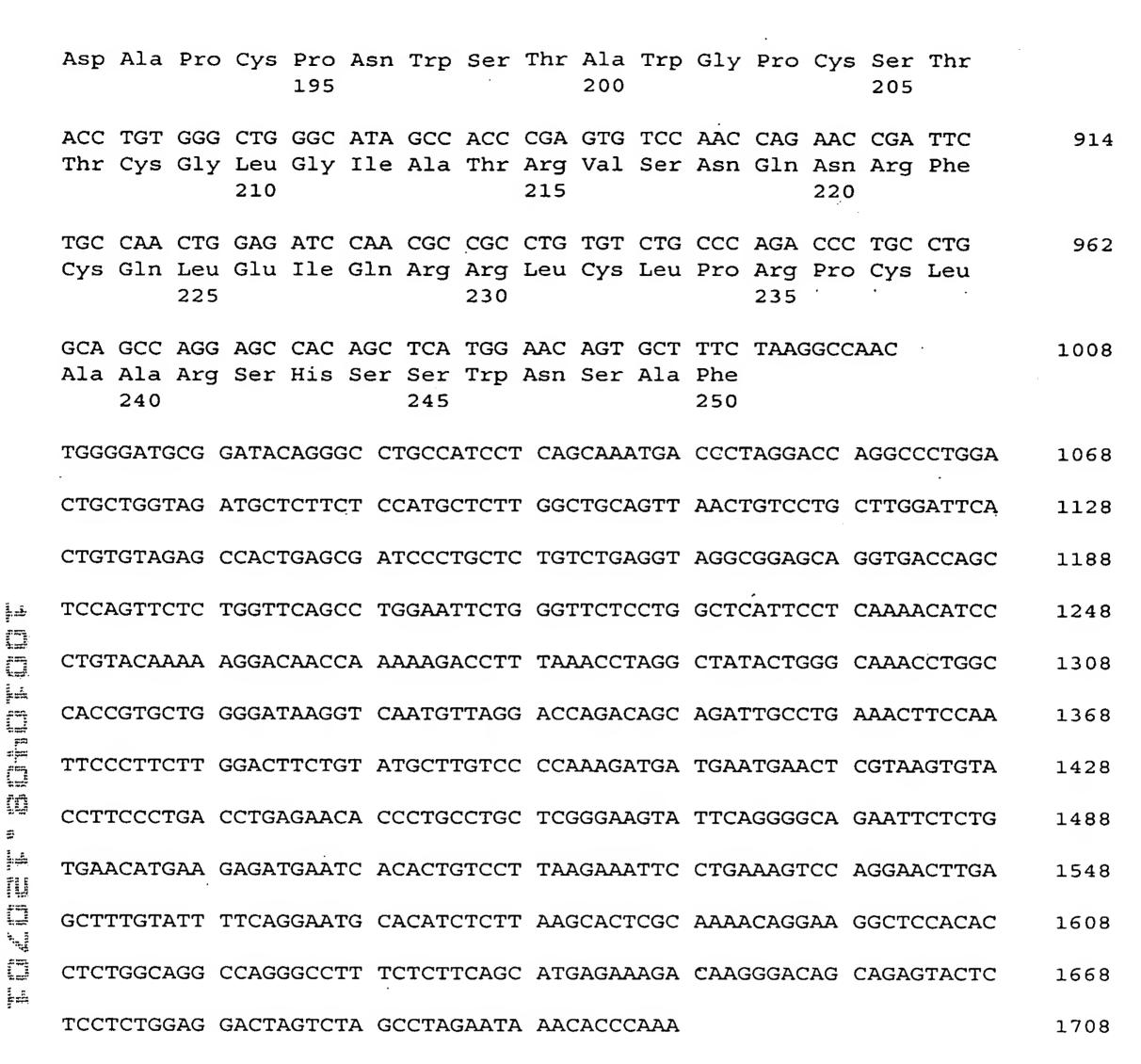
Neeotide and Amino Acid Sequences of RandiCP

GACGCTTCTG ATCTCCAGAG GACCCTGGGG TGGGACAGGG GCCTTGGCAA GGCTGCAGCC	60
GCTGGGCAGT GGCTTGGAAT GGAGGTCTTT ATTACTGGGA ACTGAGGAGC TAAGAGGCTC	120
CTGTCAGCTT GTCCTAAAGT CTTAGCACTT GTGGTGGCTT GGGCTTCACA CACTGTCAGA	180
CACCTTCGTG GTGGCCTCCA CGGCCTCACC TTCAGGTTTG AAGCTGGCTC CACAAGGGAC	240
ACGGTGAC ATG AGG GGC AGC CCA CTG ATC CAT CTT CTG GCC ACT TCC TTC Met Arg Gly Ser Pro Leu Ile His Leu Leu Ala Thr Ser Phe 1 5 10	290
CTC TGC CTT CTC TCA ATG GTG TGT GCC CAG CTG TGC CGG ACA CCC TGT Leu Cys Leu Leu Ser Met Val Cys Ala Gln Leu Cys Arg Thr Pro Cys 25 30	338
ACC TGT CCT TGG ACA CCA CCC CAG TGC CCA CAG GGG GTA CCC CTG GTG Thr Cys Pro Trp Thr Pro Pro Gln Cys Pro Gln Gly Val Pro Leu Val 35 40 45	386
CTG GAT GGC TGT GGC TGT AAA GTG TGT GCA CGG AGG CTG GGG GAG Leu Asp Gly Cys Gly Cys Lys Val Cys Ala Arg Arg Leu Gly Glu 50 55 60	434
TCC TGC GAC CAC CTG CAT GTC TGC GAC CCC AGC CAG GGC CTG GTT TGT Ser Cys Asp His Leu His Val Cys Asp Pro Ser Gln Gly Leu Val Cys 65 70 75	482
CAG CCT GGG GCA GGC CCT GGC GGC CAT GGG GCT GTG TGT CTC TTG GAT Gln Pro Gly Ala Gly Pro Gly Gly His Gly Ala Val Cys Leu Leu Asp 80 85 90	530
GAG GAT GAC GGT AGC TGT GAG GTG AAT GGC CGC AGG TAC CTG GAT GGA Glu Asp Asp Gly Ser Cys Glu Val Asn Gly Arg Arg Tyr Leu Asp Gly 95 100 105 110	578
GAG ACC TTT AAA CCC AAT TGC AGG GTC CTG TGC CGC TGT GAT GAC GGT Glu Thr Phe Lys Pro Asn Cys Arg Val Leu Cys Arg Cys Asp Asp Gly 115 120 125	626
GGC TTC ACC TGC CTG CCG CTG TGC AGT GAG GAT GTG CGG CTG CCC AGC Gly Phe Thr Cys Leu Pro Leu Cys Ser Glu Asp Val Arg Leu Pro Ser 130 140	674
TGG GAC TGC CCA CGC CCC AAG AGA ATA CAG GTG CCA GGA AAG TGC TGC Trp Asp Cys Pro Arg Pro Lys Arg Ile Gln Val Pro Gly Lys Cys 145 150 155	722
CCC GAG TGG GTA TGT GAC CAG GGA GTG ACA CCG GCG ATC CAG CGC TCC Pro Glu Trp Val Cys Asp Gln Gly Val Thr Pro Ala Ile Gln Arg Ser 160 165 170	770
ACG GCG CAA GGA CAC CAA CTT TCT GCC CTT GTC ACT CCT GCC TCT GCT Thr Ala Gln Gly His Gln Leu Ser Ala Leu Val Thr Pro Ala Ser Ala 175 180 185 190	818
GAT GCT CCT TGT CCA AAT TGG AGC ACA GCC TGG GGC CCC TGC TCA ACC	866



Nucleotide Sequence Incoding Mature HICP and the Amine Ind Sequence of Mature HICP

									CCT Pro 10							48
									GGC Gly							96
									GAC Asp							144
									GGG Gly							192
									GAC Asp							240
Gly	Arg	Arg	Tyr	Leu 85	Asp	Gly	Glu	Thr	TTT Phe 90	Lys	Pro	Asn	Cys	Arg 95	Val	288
Leu	Cys	Arg	Cys 100	Asp	Asp	Gly	Gly	Phe 105	ACC Thr	Cys	Leu	Pro	Leu 110	Cys	Ser	336
Glu	Asp	Val 115	Arg	Leu	Pro	Ser	Trp 120	Asp	TGC Cys	Pro	Arg	Pro 125	Lys	Arg	Ile	384
Gln	Val 130	Pro	Gly	Lys	Cys	Cys 135	Pro	Glu	TGG Trp	Val	Cys 140	Asp	Gln	Gly	Val	432
Thr 145	Pro	Ala	Ile	Gln	Arg 150	Ser	Thr	Ala	CAA Gln	Gly 155	His	Gln	Leu	Ser	Ala 160	480
Leu	Val	Thr	Pro	Ala 165	Ser	Ala	Asp	Ala	Pro 170	Cys	Pro	Asn	Trp	Ser 175	Thr	528
Ala	Trp	Gly	Pro 180	Cys	Ser	Thr	Thr	Cys 185	GGG Gly	Leu	Gly	Ile	Ala 190	Thr	Arg	576
Val	Ser	Asn 195	Gln	Asn	Arg	Phe	Cys 200	Gln	CTG Leu	Glu	Ile	Gln 205	Arg	Arg	Leu	624
									AGG Arg							672

AGT GCT TTC Ser Ala Phe 225

Alignment of the Modular Domains of HICP with the Modular Domains of Other **CCN Family Members**

MODULE I : IGFBP Domain

•	•		•		
100	PGGHGAVÇLL	ANRKIGVCTA	PNNOTGICMV	KGIÇRA	*
90 91	PGGH	ANRK	PNNQ	STAL	•• •
	VCDPSQGLVCQPGAG	PCDPHKGLFCDFGSP		PCDHTKGLECNFGAS	* * *
11 75 76	CARLGESCDHLH	RVCAKQLGELCTERD PO			* * **
60 61	S K	S S	C	C R	*
	OGVPLVLDGCG	-PAGVSLVLDGCGCC	AP-GVRSVLDGCSC	AP-GVGLVRDGCGCC	***
45 46	OT COMPONENT PROCE	ODC SOCIO - CAREAPHC	I REPSECEPTION TO THE PARCENT OF THE	VR61 -TCPAACHCPLEA-PKC	* . * . *
			2 CIGE	2 (+ 0111) T

MODULE II : vWFC Domain

180				DEDSTRUSTING	
166); (2:12 2:13) C); (= :), >,` × `	
51 165 payor Over 70 165	ሊ . ር		AFRAVAV FGECCE	NPRLVKVSGQCCEE	* * * * .
150 1	ר ה הני	ַל. ל היינו	יי טיי מיין	LGC P	*
136	DVKLPS	ال الا	_	IPLCPOELSLPN	*
. 135	NCRVLCRCDDGGFTC	SCKYQCTCLDGAVGC	NCQYFCTCRDGQIGC	NCKHQCTCIDGAVGC	* * * *
101 120 121		DGAPCVFGGSVYRSGESFQS	EGDNCVFDGVIYRNGEKFEP		*
	1 HICP	2 CTGF	3 NOV	4 CYR61	

MODULE III : TSP1 Domain

280 LPRPCLAARSHSSWNSAF- MVRPCEADLEENIK-KGKK IVRPCEQEPEEVTDKKGKK EVRPCGQPVYSSLK-KGKK
265 NONRFCQLEIQRRLC NDNTFCRLEKQSRLC NRNRQCEMVKQTRLC NDNPECRLVKETRIC *
250 PCSTTCGLGIATRVS ACSKTCGMGISTRVT ACSKSCGMGVSTRVT QCSKSCGTGISTRVT
240 PCPNWSTAWG NCLVQTTEWS NCIEQTTEWS KCIVQTTSWS
1 HICP 2 CTGF 3 NOV 4 CYR61

Northern Blot Analysis of HICP Expression in Rat Aorta Smooth Muscle Cells

